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SEQUENCE LISTING

<110> Ishihara Sangyo Kaisha, Ltd.
 <120> Regulation of RAPL-Rap1 Interaction
 <130> IS-08PCT
 <150> JP 2002-316892
 <151> 2002-10-30
 <160> 14
 <170> PatentIn version 3.1
 <210> 1
 <211> 555
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (1)..(555)
 <223> Human Rap1

<400> 1
 atg cgt gag tac aag cta gtg gtc ctt ggt tca gga ggc gtt ggg aag 48
 Met Arg Glu Tyr Lys Leu Val Val Leu Gly Ser Gly Gly Val Gly Lys
 1 5 10 15
 tct gct ctg aca gtt cag ttt gtt cag gga att ttt gtt gaa aaa tat 96
 Ser Ala Leu Thr Val Gln Phe Val Gln Gly Ile Phe Val Glu Lys Tyr
 20 25 30
 gac cca acg ata gaa gat tcc tac aga aag caa gtt gaa gtc gat tgc 144
 Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Glu Val Asp Cys
 35 40 45
 caa cag tgt atg ctc gaa atc ctg gat act gca ggg aca gag caa ttt 192
 Gln Gln Cys Met Leu Glu Ile Leu Asp Thr Ala Gly Thr Glu Gln Phe
 50 55 60
 aca gca atg agg gat ttg tat atg aag aac ggc caa ggt ttt gca cta 240
 Thr Ala Met Arg Asp Leu Tyr Met Lys Asn Gly Gln Gly Phe Ala Leu
 65 70 75 80
 gta tat tct att aca gct cag tcc acg ttt aac gac tta cag gac ctg 288
 Val Tyr Ser Ile Thr Ala Gln Ser Thr Phe Asn Asp Leu Gln Asp Leu
 85 90 95
 agg gaa cag att tta cgg gtt aag gac acg gaa gat gtt cca atg att 336
 Arg Glu Gln Ile Leu Arg Val Lys Asp Thr Glu Asp Val Pro Met Ile
 100 105 110
 ttg gtt ggc aat aaa tgt gac ctg gaa gat gag cga gta gtt ggc aaa 384
 Leu Val Gly Asn Lys Cys Asp Leu Glu Asp Glu Arg Val Val Gly Lys

115	120	125	
gag cag ggc cag aat tta Glu Gln Gly Gln Asn Leu 130	gca aga cag tgg tgt Ala Arg Gln Trp Cys 135	aac tgt gcc ttt tta Asn Cys Ala Phe Leu 140	432
gaa tct tct gca aag tca Glu Ser Ser Ala Lys Ser 145	aag atc aat gtt aat Lys Ile Asn Val Asn 150	gag ata ttt tat gac Glu Ile Phe Tyr Asp 155	480
ctg gtc aga cag ata aat Leu Val Arg Gln Ile 165	agg aaa aca cca Arg Lys Thr Pro 170	gtg gaa aag aag aag cct Val Glu Lys Lys Lys Pro 175	528
aaa aag aaa tca tgt Lys Lys Lys Ser Cys 180	ctg ctg ctc tag Leu Leu Leu		555

<210> 2
 <211> 184
 <212> PRT
 <213> Homo sapiens

<400> 2

Met Arg Glu Tyr Lys Leu Val Val Leu Gly Ser Gly Gly Val Gly Lys 1 5 10 15
Ser Ala Leu Thr Val Gln Phe Val Gln Gly Ile Phe Val Glu Lys Tyr 20 25 30
Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Glu Val Asp Cys 35 40 45
Gln Gln Cys Met Leu Glu Ile Leu Asp Thr Ala Gly Thr Glu Gln Phe 50 55 60
Thr Ala Met Arg Asp Leu Tyr Met Lys Asn Gly Gln Gly Phe Ala Leu 65 70 75 80
Val Tyr Ser Ile Thr Ala Gln Ser Thr Phe Asn Asp Leu Gln Asp Leu 85 90 95
Arg Glu Gln Ile Leu Arg Val Lys Asp Thr Glu Asp Val Pro Met Ile 100 105 110
Leu Val Gly Asn Lys Cys Asp Leu Glu Asp Glu Arg Val Val Gly Lys 115 120 125

Glu Gln Gly Gln Asn Leu Ala Arg Gln Trp Cys Asn Cys Ala Phe Leu
 130 135 140

Glu Ser Ser Ala Lys Ser Lys Ile Asn Val Asn Glu Ile Phe Tyr Asp
 145 150 155 160

Leu Val Arg Gln Ile Asn Arg Lys Thr Pro Val Glu Lys Lys Lys Pro
 165 170 175

Lys Lys Lys Ser Cys Leu Leu Leu
 180

<210> 3
 <211> 798
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(798)
 <223> Human RAPL (or Human p30)

<400> 3
 atg acc gtg gac agc agc atg agc agt ggg tac tgc agc ctg gac gag 48
 Met Thr Val Asp Ser Ser Met Ser Ser Gly Tyr Cys Ser Leu Asp Glu
 1 5 10 15
 gaa ctg gaa gac tgc ttc ttc act gct aag act acc ttt ttc aga aat 96
 Glu Leu Glu Asp Cys Phe Phe Thr Ala Lys Thr Thr Phe Phe Arg Asn
 20 25 30
 gcg cag agc aaa cat ctt tca aag aat gtc tgt aaa cct gtg gag gaa 144
 Ala Gln Ser Lys His Leu Ser Lys Asn Val Cys Lys Pro Val Glu Glu
 35 40 45
 aca cag cgc ccg ccc aca ctg cag gag atc aag cag aag atc gac agc 192
 Thr Gln Arg Pro Pro Thr Leu Gln Glu Ile Lys Gln Lys Ile Asp Ser
 50 55 60
 tac aac acg cga gag aag aac tgc ctg ggc atg aaa ctg agt gaa gac 240
 Tyr Asn Thr Arg Glu Lys Asn Cys Leu Gly Met Lys Leu Ser Glu Asp
 65 70 75 80
 ggc acc tac acg ggt ttc atc aaa gtg cat ctg aaa ctc cgg cgg cct 288
 Gly Thr Tyr Thr Gly Phe Ile Lys Val His Leu Lys Leu Arg Arg Pro
 85 90 95
 gtg acg gtg cct gct ggg atc cgg ccc cag tcc atc tat gat gcc atc 336
 Val Thr Val Pro Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile
 100 105 110
 aag gag gtg aac ctg gcg gct acc acg gac aag cgg aca tcc ttc tac 384
 Lys Glu Val Asn Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr

115	120	125	
ctg ccc cta gat gcc atc aag cag ctg cac atc agc agc acc acc acc Leu Pro 130 Leu Asp Ala Ile Lys 135 Gln Leu His Ile Ser Ser Thr Thr Thr			432
gtc agt gag gtc atc cag ggg ctg ctc aag aag ttc atg gtt gtg gac Val Ser Glu Val Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp 145 150 155 160			480
aat ccc cag aag ttt gca ctt ttt aag cgg ata cac aag gac gga caa Asn Pro Gln Lys Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln 165 170 175			528
gtg ctc ttc cag aaa ctc tcc att gct gac cgc ccc ctc tac ctg cgc Val Leu Phe Gln Lys Leu Ser Ile Ala Asp Arg Pro Leu Tyr Leu Arg 180 185 190			576
ctg ctt gct ggg cct gac acg gag gtc ctc agc ttt gtg cta aag gag Leu Leu Ala Gly Pro Asp Thr Glu Val Leu Ser Phe Val Leu Lys Glu 195 200 205			624
aat gaa act gga gag gta gag tgg gat gcc ttc tcc atc cct gaa ctt Asn Glu Thr Gly Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu 210 215 220			672
cag aac ttc cta aca atc ctg gaa aaa gag gag cag gac aaa atc caa Gln Asn Phe Leu Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile Gln 225 230 235 240			720
caa gtg caa aag aag tat gac aag ttt agg cag aaa ctg gag gag gcc Gln Val Gln Lys Lys Tyr Asp Lys Phe Arg Gln Lys Leu Glu Glu Ala 245 250 255			768
tta aga gaa tcc cag ggc aaa cct ggg taa Leu Arg Glu Ser Gln Gly Lys Pro Gly 260 265			798

<210> 4
 <211> 265
 <212> PRT
 <213> Homo sapiens

<400> 4

Met Thr Val Asp Ser Ser Met Ser Ser Gly Tyr Cys Ser Leu Asp Glu 1 5 10 15	
Glu Leu Glu Asp Cys Phe Phe Thr Ala Lys Thr Thr Phe Phe Arg Asn 20 25 30	
Ala Gln Ser Lys His Leu Ser Lys Asn Val Cys Lys Pro Val Glu Glu 35 40 45	

Thr Gln Arg Pro Pro Thr Leu Gln Glu Ile Lys Gln Lys Ile Asp Ser
 50 55 60
 Tyr Asn Thr Arg Glu Lys Asn Cys Leu Gly Met Lys Leu Ser Glu Asp
 65 70 75 80
 Gly Thr Tyr Thr Gly Phe Ile Lys Val His Leu Lys Leu Arg Arg Pro
 85 90 95
 Val Thr Val Pro Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile
 100 105 110
 Lys Glu Val Asn Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr
 115 120 125
 Leu Pro Leu Asp Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr
 130 135 140
 Val Ser Glu Val Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp
 145 150 155 160
 Asn Pro Gln Lys Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln
 165 170 175
 Val Leu Phe Gln Lys Leu Ser Ile Ala Asp Arg Pro Leu Tyr Leu Arg
 180 185 190
 Leu Leu Ala Gly Pro Asp Thr Glu Val Leu Ser Phe Val Leu Lys Glu
 195 200 205
 Asn Glu Thr Gly Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu
 210 215 220
 Gln Asn Phe Leu Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile Gln
 225 230 235 240
 Gln Val Gln Lys Lys Tyr Asp Lys Phe Arg Gln Lys Leu Glu Glu Ala
 245 250 255
 Leu Arg Glu Ser Gln Gly Lys Pro Gly
 260 265

<210> 5
 <211> 498

<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(498)
 <223> Dominant-Negative Human RAPL

<400> 5
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 Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile Lys Glu Val Asn
 1 5 10 15
 ctg gcg gct acc acg gac aag cgg aca tcc ttc tac ctg ccc cta gat 96
 Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr Leu Pro Leu Asp
 20 25 30
 gcc atc aag cag ctg cac atc agc agc acc acc acc gtc agt gag gtc 144
 Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr Val Ser Glu Val
 35 40 45
 atc cag ggg ctg ctc aag aag ttc atg gtt gtg gac aat ccc cag aag 192
 Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp Asn Pro Gln Lys
 50 55 60
 ttt gca ctt ttt aag cgg ata cac aag gac gga caa gtg ctc ttc cag 240
 Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln Val Leu Phe Gln
 65 70 75 80
 aaa ctc tcc att gct gac cgc ccc ctc tac ctg cgc ctg ctt gct ggg 288
 Lys Leu Ser Ile Ala Asp Arg Pro Leu Tyr Leu Arg Leu Leu Ala Gly
 85 90 95
 cct gac acg gag gtc ctc agc ttt gtg cta aag gag aat gaa act gga 336
 Pro Asp Thr Glu Val Leu Ser Phe Val Leu Lys Glu Asn Glu Thr Gly
 100 105 110
 gag gta gag tgg gat gcc ttc tcc atc cct gaa ctt cag aac ttc cta 384
 Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu Gln Asn Phe Leu
 115 120 125
 aca atc ctg gaa aaa gag gag cag gac aaa atc caa caa gtg caa aag 432
 Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile Gln Gln Val Gln Lys
 130 135 140
 aag tat gac aag ttt agg cag aaa ctg gag gag gcc tta aga gaa tcc 480
 Lys Tyr Asp Lys Phe Arg Gln Lys Leu Glu Glu Ala Leu Arg Glu Ser
 145 150 155 160
 cag ggc aaa cct ggg taa 498
 Gln Gly Lys Pro Gly
 165

<210> 6
 <211> 165
 <212> PRT

<213> Homo sapiens

<400> 6

Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile Lys Glu Val Asn
1 5 10 15

Leu Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr Leu Pro Leu Asp
20 25 30

Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr Val Ser Glu Val
35 40 45

Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp Asn Pro Gln Lys
50 55 60

Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln Val Leu Phe Gln
65 70 75 80

Lys Leu Ser Ile Ala Asp Arg Pro Leu Tyr Leu Arg Leu Leu Ala Gly
85 90 95

Pro Asp Thr Glu Val Leu Ser Phe Val Leu Lys Glu Asn Glu Thr Gly
100 105 110

Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu Gln Asn Phe Leu
115 120 125

Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile Gln Gln Val Gln Lys
130 135 140

Lys Tyr Asp Lys Phe Arg Gln Lys Leu Glu Glu Ala Leu Arg Glu Ser
145 150 155 160

Gln Gly Lys Pro Gly
165

<210> 7

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Nucleotide Sequence for Myc-tag

<400> 7

atggaacaga aactcatatc ggaggaggat cta

<210> 8
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Peptide Sequence for Myc-tag

<400> 8

Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
 1 5 10

<210> 9
 <211> 798
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(798)
 <223> House Mouse RAPL (Region 104 to 901 of mRNA)

<400> 9

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Met Thr Val Asp Ser Ser Met Ser Ser Gly Tyr Cys Ser Leu Asp Glu	
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gaa ctg gaa gat tgc ttc ttt acg gct aag acc acc ttc ttc agg aat	96
Glu Leu Glu Asp Cys Phe Phe Thr Ala Lys Thr Thr Phe Phe Arg Asn	
20 25 30	
ctt cag agc aaa cag cct tca aag aat gtc tgt aag gca gtg gag gag	144
Leu Gln Ser Lys Gln Pro Ser Lys Asn Val Cys Lys Ala Val Glu Glu	
35 40 45	
aca cag cac ccg ccc acg ata cag gag atc aag cag aag att gac agc	192
Thr Gln His Pro Pro Thr Ile Gln Glu Ile Lys Gln Lys Ile Asp Ser	
50 55 60	
tat aac agc agg gag aag cac tgc ctg ggc atg aag ctg agt gaa gat	240
Tyr Asn Ser Arg Glu Lys His Cys Leu Gly Met Lys Leu Ser Glu Asp	
65 70 75 80	
ggc acc tac aca ggt ttc atc aaa gtg cat ttg aag ctc cga cgg cca	288
Gly Thr Tyr Thr Gly Phe Ile Lys Val His Leu Lys Leu Arg Arg Pro	
85 90 95	
gtg acg gtg ccc gct ggg atc cgg ccc cag tcc atc tat gat gcc att	336
Val Thr Val Pro Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile	
100 105 110	
aag gaa gtg aac cct gca gcc acc aca gac aag cgg act tcc ttc tac	384
Lys Glu Val Asn Pro Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr	

115	120	125	
ctg cca ctc gat gcc atc aag cag cta cat atc agc agc acc acc acg Leu Pro Leu Asp Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr 130 135 140			432
gtt agt gag gtc atc cag ggg ctg ctc aag aag ttc atg gtt gtg gac Val Ser Glu Val Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp 145 150 155 160			480
aac cca cag aag ttt gca ctt ttt aag cgg ata cac aaa gat gga caa Asn Pro Gln Lys Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln 165 170 175			528
gtg ctc ttc cag aaa ctc tcc att gct gac tat cct ctc tac ctt cgt Val Leu Phe Gln Lys Leu Ser Ile Ala Asp Tyr Pro Leu Tyr Leu Arg 180 185 190			576
ctg ctc gct ggg cct gac acc gat gtt ctc agc ttt gtg cta aag gag Leu Leu Ala Gly Pro Asp Thr Asp Val Leu Ser Phe Val Leu Lys Glu 195 200 205			624
aat gaa act gga gag gtg gag tgg gat gcc ttt tcc att cct gaa ctc Asn Glu Thr Gly Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu 210 215 220			672
cag aac ttt tta act atc ctg gaa aaa gag gag cag gac aag atc cat Gln Asn Phe Leu Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile His 225 230 235 240			720
caa ctg caa aag aag tac aac aaa ttc cgt cag aaa ctg gaa gag gca Gln Leu Gln Lys Lys Tyr Asn Lys Phe Arg Gln Lys Leu Glu Glu Ala 245 250 255			768
tta cga gag tcc caa ggg aag ccg ggg taa Leu Arg Glu Ser Gln Gly Lys Pro Gly 260 265			798

<210> 10
 <211> 265
 <212> PRT
 <213> Mus musculus

<400> 10

Met Thr Val Asp Ser Ser Met Ser Ser Gly Tyr Cys Ser Leu Asp Glu
1 5 10 15

Glu Leu Glu Asp Cys Phe Phe Thr Ala Lys Thr Thr Phe Phe Arg Asn
20 25 30

Leu Gln Ser Lys Gln Pro Ser Lys Asn Val Cys Lys Ala Val Glu Glu
35 40 45

Thr Gln His Pro Pro Thr Ile Gln Glu Ile Lys Gln Lys Ile Asp Ser
 50 55 60

Tyr Asn Ser Arg Glu Lys His Cys Leu Gly Met Lys Leu Ser Glu Asp
 65 70 75 80

Gly Thr Tyr Thr Gly Phe Ile Lys Val His Leu Lys Leu Arg Arg Pro
 85 90 95

Val Thr Val Pro Ala Gly Ile Arg Pro Gln Ser Ile Tyr Asp Ala Ile
 100 105 110

Lys Glu Val Asn Pro Ala Ala Thr Thr Asp Lys Arg Thr Ser Phe Tyr
 115 120 125

Leu Pro Leu Asp Ala Ile Lys Gln Leu His Ile Ser Ser Thr Thr Thr
 130 135 140

Val Ser Glu Val Ile Gln Gly Leu Leu Lys Lys Phe Met Val Val Asp
 145 150 155 160

Asn Pro Gln Lys Phe Ala Leu Phe Lys Arg Ile His Lys Asp Gly Gln
 165 170 175

Val Leu Phe Gln Lys Leu Ser Ile Ala Asp Tyr Pro Leu Tyr Leu Arg
 180 185 190

Leu Leu Ala Gly Pro Asp Thr Asp Val Leu Ser Phe Val Leu Lys Glu
 195 200 205

Asn Glu Thr Gly Glu Val Glu Trp Asp Ala Phe Ser Ile Pro Glu Leu
 210 215 220

Gln Asn Phe Leu Thr Ile Leu Glu Lys Glu Glu Gln Asp Lys Ile His
 225 230 235 240

Gln Leu Gln Lys Lys Tyr Asn Lys Phe Arg Gln Lys Leu Glu Glu Ala
 245 250 255

Leu Arg Glu Ser Gln Gly Lys Pro Gly
 260 265

<210> 11
 <211> 30

<212> DNA
 <213> Artificial Sequence
 <220>
 <223> Oligonucleotide to act as a primer for PCR
 <400> 11
 atgaccgtgg acagcagcat gagcagcggg 30

<210> 12
 <211> 30
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Oligonucleotide to act as a primer for PCR
 <400> 12
 tatttgtgag ccagggcatt ggccacacca 30

<210> 13
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Oligonucleotide to act as a primer for PCR
 <400> 13
 atcaattacg gggtcattag 20

<210> 14
 <211> 20
 <212> DNA
 <213> Artificial Sequence
 <220>
 <223> Oligonucleotide to act as a primer for PCR
 <400> 14
 tgtactgcca agtaggaaag 20